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<170> PatentIn Ver. 2.1

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<222> (232)..(1161)

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tagtaaaatg ttagaaatag ctgttttga ttcactttgt gcatgttaggc t gtg acc 237
Met Thr
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atg ggc aac gac ggc gga gac ctg cga atc gac gac cta cgc agc ttc 285
Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
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att tca gtc gct caa tca ggc cac ctc acc gaa act gcc gaa aga tta 333
Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu Arg Leu
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cac gca ggc acc cca ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc 429
His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
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Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
70 75 80gaa ttc aac tcc gcc gca act gaa atc aaa cgc ctc atg gac cca gaa 525
Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
85 90 95

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Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala	
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35 ggt ttc ggc acc cga ctc ctc atg gat gca tta gcc gaa gaa gcc ggt	909
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215 220 225	
40 ttt gtt ccc aat gtg gtt ttc gaa tcc atg gaa ctc acc acc gtc gca	957
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Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro	
260 265 270	
55 gct tat agg gaa cta ggt ttg gtg tgg cga ctc aac gcg ggg ccg gca	1101
Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly Pro Ala	
275 280 285 290	
50 cct gcg gtg gat aac ttc cgg aag ttc gtg gcg gga tcg agg tat gca	1149
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115 120 125

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Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
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50 Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
210 215 220

Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
55 225 230 235 240

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 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
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The following figures are attached:

Figure 1: Map of the plasmid pCR2.1lysR2int.

The abbreviations and designations used have the following meaning.

KmR: Kanamycin resistance gene

EcoRI: Cleavage site of the restriction enzyme EcoRI

lysR2int: Internal fragment of the lysR2 gene

ColE1 ori: Replication origin of the plasmid ColE1

SEQUENZPROTOKOLL

<110> Degussa AG

5 <120> Neue für das lysR2-Gen kodierende Nukleotidsequenzen

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15 <170> PatentIn Ver. 2.1

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cctcgacctt gctatctatt gcttggctca tggagttcat catgcgccaa cagcaaataat 180

tagtaaaatg ttagaaatag ctgttttga ttcactttgt gcatgttaggc t gtg acc 237
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Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe

5

10

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His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
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Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
85 90 95

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Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met		
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Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro		
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Leu Glu Glu Gly		
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Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
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45 Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln
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Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met
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50 Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
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Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
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Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met
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Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser
 260 265 270

5 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
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